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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,234

DATE: 08/28/2001

TIME: 11:57:30

Input Set : A:\98385Iseq.txt

Output Set: N:\CRF3\08282001\I898234.raw

ENTERED

p. 5

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmeler, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
9 Them
11 <130> FILE REFERENCE: 98,385-I
14 <140> CURRENT APPLICATION NUMBER: 09/898,234
15 <141> CURRENT FILING DATE: 2001-07-03
17 <150> PRIOR APPLICATION NUMBER: 09/525,998
18 <151> PRIOR FILING DATE: 2000-03-15
20 <150> PRIOR APPLICATION NUMBER: 08/383,676
21 <151> PRIOR FILING DATE: 1995-02-01
23 <150> PRIOR APPLICATION NUMBER: 08/153,287
24 <151> PRIOR FILING DATE: 1993-11-17
26 <150> PRIOR APPLICATION NUMBER: 07/821,750
27 <151> PRIOR FILING DATE: 1992-01-02
29 <150> PRIOR APPLICATION NUMBER: 07/511,430
30 <151> PRIOR FILING DATE: 1990-04-20
32 <160> NUMBER OF SEQ ID NOS: 87
34 <170> SOFTWARE: PatentIn Ver. 2.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1368
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
41 <220> FEATURE:
42 <221> NAME/KEY: CDS
43 <222> LOCATION: (1)..(1368)
45 <220> FEATURE:
46 <221> NAME/KEY: sig_peptide
47 <222> LOCATION: (1)..(87)
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (88)..(120)
52 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
53 extracellular proteases following secretion.
55 <220> FEATURE:
56 <221> NAME/KEY: misc_feature
57 <222> LOCATION: (606)..(633)
58 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
59 extracellular proteases following secretion.
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63 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
64 1 5 10 15
66 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
67 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

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68	20	25	30	
70	cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa	144		
71	His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys			
72	35 40 45			
74	tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa	192		
75	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys			
76	50 55 60			
78	gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac	240		
79	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp			
80	65 70 75 80			
82	tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc	288		
83	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu			
84	85 90 95			
86	aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg	336		
87	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val			
88	100 105 110			
90	gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384		
91	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg			
92	115 120 125			
94	aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432		
95	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe			
96	130 135 140			
98	aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag	480		
99	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
100	145 150 155 160			
102	aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa	528		
103	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
104	165 170 175			
106	aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg	576		
107	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
108	180 185 190			
110	aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624		
111	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
112	195 200 205			
114	ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672		
115	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
116	210 215 220			
118	tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag	720		
119	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
120	225 230 235 240			
122	tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag	768		
123	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
124	245 250 255			
126	ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc	816		
127	Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
128	260 265 270			
130	ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg	864		
131	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
132	275 280 285			

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134 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
135 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
136 290 295 300
138 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
139 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
140 305 310 315 320
142 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
143 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
144 325 330 335
146 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
147 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
148 340 345 350
150 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
151 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
152 355 360 365
154 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
155 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
156 370 375 380
158 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
159 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
160 385 390 395 400
162 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
163 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
164 405 410 415
166 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
167 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
168 420 425 430
170 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
171 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
172 435 440 445
174 ccc gcg ccc agt ctt ctc aga tga 1368
175 Pro Ala Pro Ser Leu Leu Arg
176 450 455
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 455
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 2
185 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
186 1 5 10 15
188 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
189 20 25 30
191 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
192 35 40 45
194 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
195 50 55 60
197 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
198 65 70 75 80
200 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu

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Input Set : A:\98385Iseq.txt

Output Set: N:\CRF3\08282001\I898234.raw

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201          85          90          95
203 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
204          100          105          110
206 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
207          115          120          125
209 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
210          130          135          140
212 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
213 145          150          155          160
215 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
216          165          170          175
218 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
219          180          185          190
221 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
222          195          200          205
224 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
225          210          215          220
227 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
228 225          230          235          240
230 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
231          245          250          255
233 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
234          260          265          270
236 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
237          275          280          285
239 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
240          290          295          300
242 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
243 305          310          315          320
245 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
246          325          330          335
248 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
249          340          345          350
251 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
252          355          360          365
254 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
255          370          375          380
257 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
258 385          390          395          400
260 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
261          405          410          415
263 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
264          420          425          430
266 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
267          435          440          445
269 Pro Ala Pro Ser Leu Leu Arg
270          450          455
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 483

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RAW SEQUENCE LISTING

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Input Set : A:\98385Iseq.txt

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275 <212> TYPE: DNA
276 <213> ORGANISM: Homo sapiens
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (1)..(483)
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284 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
285   1           5           10           15
287 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
288 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
289           20           25           30
291 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc      144
292 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
293           35           40           45
295 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa      192
296 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
297           50           55           60
299 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac      240
300 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
301 65           70           75           80
303 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg      288
304 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
305           85           90           95
307 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg      336
308 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
309           100          105          110
311 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc      384
312 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
313           115          120          125
315 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac      432
316 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
317           130          135          140
319 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag      480
320 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
321 145          150          155          160
323 aat                                                                 483
324 Asn
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 161
329 <212> TYPE: PRT
330 <213> ORGANISM: Homo sapiens
332 <400> SEQUENCE: 4
333 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
334   1           5           10           15
336 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
337           20           25           30
339 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
340           35           40           45

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/898,234

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Input Set : A:\98385Iseq.txt

Output Set: N:\CRF3\08282001\I898234.raw

L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36